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Database :
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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A_Geneseq_0601:*

1: \SIDS8\gcgdata\geneseq\geneseq\paa1980.DaT:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1 1641 100.0 2 1641 100.0 3 1349 82.2 4 1215 74.0 5 1215 74.0 6 1213 73.9 7 1213 73.9 8 1213 73.9 9 916 53.6 11 849.5 51.8	Result Query No. Score Match Length DB
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21 21 21 21 21 21 21 21 21 21 21	DB
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XX	18-OCT-2000 (first entry)
XX DE	Arabidopsis thaliana protein fragment SEQ ID NO: 57548.
ΚW	Protein identification; signal transduction nothway, metabolic mathematical
KW	
XX	termination sequence.
XX SO	Arabidopsis thaliana.
X PN	EP1033405-A2.
XX D	06-SEP-2000.
PF XX	25-FEB-2000; 2000EP-0301439.
PR	25-FEB-1999; 99US-0121825.
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                                               Arabidopsis thaliana.
                                                             glutathione; methionine; nutri
glutathione; viral resistance.
                                                                                                           03-OCT-2000 (first entry)
                                                                                                                                            AAY93901 standard; Protein;
                                                                                           Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3
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                                                                                                                                                                                                                                                                                                                                                              MATCIDTCRTGNTQDDDSRFCCIKNFFRPGFSVNRKIHHTQIEDDDDVWIKMLEEAKSDV
                                                                            acetyltransferase; SAT;
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990S-0161404
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Pred. No. 2e-151;
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lue; plant-derived
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Best Local Similarity
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                                  Protein identification; signal transduction pathway; metabolic pathway; hwhridication assav: denetic mapping; gene emersion control; promoter;
                                                                          Arabidopsis thaliana protein fragment SEQ ID .): 57549
                                                                                                         18-OCT-2000
                                                                                                                                                          AAG45803 standard; Protein;
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Arabidopsis thaliana termination sequence

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99US-0139454. 99US-0139456. 99US-0139457. 99US-0139459. 99US-0139469. 99US-0139462. 99US-0139462. 99US-0139463. 99US-0139763. 99US-0139763. 99US-0139763. 99US-0140534. 99US-0140053. 99US-01400354. 99US-01400354. 99US-01400354. 99US-01400354. 99US-01400354.	990S-0132486 990S-0132487 990S-0134256 990S-0134218 990S-013421 990S-013421 990S-013421 990S-013476 990S-013476 990S-0135124 990S-0135629 990S-0135629 990S-0136782 990S-0137722 990S-0137722 990S-0137724 990S-0138540 990S-0138540 990S-0138540 990S-013847 990S-013847 990S-013847	2000EP-0301439. 99US-0121825. 99US-0123548. 99US-0125788. 99US-0125786. 99US-0126785. 99US-0126785. 99US-01267462. 99US-0130449. 99US-0130449. 99US-0130449. 99US-0130449. 99US-01304891. 99US-0132484.
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                                                                                          HDKIPCLTMDQTSYLTEWSDYVI 314
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                                                                                                                                                                                                                      ESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLI 171
                                                                                hdkipcltmdqtsyltewsdyvi
                                                                                                                                   HPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRK
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Increasing production of sulfur-containing compounds, e.g. cysteine methionine, in plants, useful e.g. for improving nutritional value, overexpressing serine acetyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                  VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAK;GSGSVVVKDVPARTTAVGN
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parllggkdnpkthdkipgltmdqtshisewsdyvi
                           PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI
                                                     vtlggtgkqcgdrhpkigdgvligagtcilgnitigegal.igagsvvlkdvpprttavgn
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DB; AAA47175.
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                                                                                                                                                                                                                                                                                               The present sequence represents an isoform of serine acetyltransferase (SAT). The SAT polynucleotide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine and their sulfur-containing derivatives. SAT catalyses conversion of serine to 0-acetylserine which is a precursor (by reaction with sulphide) for cysteine, itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with increased production of glutathione) to improve resistance to stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing production of sulfur-containing compounds, e.g. cysteine methionine, in plants, useful e.g. for improving nutritional value, overexpressing serine acetyltransferase \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glutathione; methionine; nutri
glutathione; viral resistance.
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                                                              SNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHT 158
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DB; AAA47176.
LWKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHG
                                         ldrdaevddvwakireeaksdiakepivsayyhasivsqrsleaalantlsvklsnlnlp
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                                                                                                                                                                                                                                                                            391
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hybridisation assay; genetic mapping; gene expression control; promoter;
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25-MAR-1999,
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01-APR-1999,
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16-APR-1999,
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23-APR-1999,
23-APR-1999,
23-APR-1999,
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Best Local Similarity
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                                                                                                                                                                                                                            Protein identification; signal transduction |\cdot|-thway; metabolic pathway; hybridisation assay; genetic mapping; gene e-cession control; promoter; termination sequence.
                                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                                                Arabidopsis thaliana.
                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID 🐠 66720.
                                                                                                                                                                                                                                                                                                                             AAG52483 standard; Protein; 1787 AA
                                                                                                                                                                                                                                                                                        18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                AAG52483;
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26-OCT-1999;
28-OCT-1999;
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                                                                                                                                                       2000EP-0301439
99US-0126264
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99US-0128234
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99US-01318449
                                                                                                       99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
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99US-0161361
99US-0161920
99US-0161920
99US-0161992
99US-0161993
99US-0162142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1213; DB 21;
Pred. No. 1.1e-108;
                                                                                                                                                                                                                                                                                                                                                                             380
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UL-1999; ULL-1999; ULL-	1-JUL-1999; 1-JUL-1999; 2-JUL-1999; 2-JUL-1999; 2-JUL-1999; 3-JUL-1999;
990S-0145218 990S-0145218 990S-0145913 990S-0145913 990S-0146388 990S-0146388 990S-0146388 990S-0147303 990S-0147260 990S-0147260 990S-0147493 990S-0147493 990S-0147493 990S-0147493 990S-0148319 990S-0148319 990S-0148319 990S-0148319 990S-0148319 990S-0148319 990S-0148319 990S-0149310 990S-0149310 990S-0149310 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151303 990S-0151333 990S-0157117 990S-0157117 990S-0157117 990S-0158029- 990S-0159239 990S-0159239 990S-0159239 990S-0159239 990S-0159330 990S-0159330 990S-0159331 990S-0159638 990S-0159638	99US-0145086. 99US-0145088. 99US-0145085. 99US-0145087. 99US-0145089. 99US-0145192. 99US-0145192.

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Best Local Similarity
Matches 240; Conserv
           25-FEB-1999;
05-MAR-1999;
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21-OCT-1999
21-OCT-1999
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28-OCT-1999
29-OCT-1999
                                    25-FEB-2000; 2000EP-0301439
                                                         06-SEP-2000
                                                                            EP1033405-A2
                                                                                               Arabidopsis thaliana
                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                      17-0CT-2000 (first entry)
                                                                                                                                                                                            AAG08083;
                                                                                                                                                                                                           AAG08083 standard; Protein; 180 AA
                                                                                                                termination sequence
                                                                                                                                                                                                                                                        279 PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
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356 parllggkdnpkthdkipgltmdqtshlsewsdyiv 391
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         99US-0121825
99US-0123180
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99US-0160767

99US-0160770

99US-0160814

99US-0160815

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99US-0161404

99US-0161406

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99US-0161361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 1213; DB 21;
; Pred. No. 1.1e-108;
33; Mismatches 41;
                                                                                                                                                   5483.
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                                                                                                                                                                                                                                                                                                                278
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01-JUL-1999
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25-MAR-1999
01-APR-1999
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16-APR-1999
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99US-0143542
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99US-0125788.
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RESULT 1
AAY44770
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PR PR N
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Best Local Similarity 97.2
Matches 175; Conservative
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07-OCT-1999;
08-OCT-1999;
12-OCT-1999;
13-OCT-1999;
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14-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
18-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
                                                                              Serine O-acetyltransferase; sulphate assimilation; O-acety soybean; clone srl.pk0162.a9; cysteine formation; marker; plant breeding; transgenic plant.
                                                               Glycine max.
                                                                                                               Soybean serine O-acetyltransferase-1.
                                                                                                                                04-MAY-2000
                                                                                                                                                AAY44770;
                                                                                                                                                               AAY44770 standard; Protein; 286 AA.
                13-JUL-1999;
14-JUL-1998;
                                 27-JAN-2000
                                               WO200004167-A2
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                                                                                                                                                                                                                                                                      990S-0157865.
990S-0158232.
990S-0158236.
990S-0159294.
990S-0159294.
990S-0159330.
990S-0159331.
990S-0159588.
990S-0159638.
990S-0160774.
990S-0160776.
990S-0160767.
990S-0160814.
990S-0160814.
990S-0160814.
990S-0160814.
990S-0160814.
990S-0161818.
                                                                                                                                (first entry)
                 99WO-US15872.
 98US-0092833
                                                                                                                                                                                                                                                                                                                55.8%;
97.2%;
                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                         Score 916; DB 21:
pred. No. 3.1e-81;
2; Mismatches 3;
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                                                                                                   O-acetylserine;
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15-JUL-1999;
16-JUL-1999;
16-JUL-1999;
19-JUL-1999;
19-JUL-1999;
19-JUL-1999;
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23-JU

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99US-0153788
99US-0153788
99US-015479
99US-0155458
99US-0155659

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is the serine O-acetyltransferase, a sulphate assimilation protein isolated from soybean. This is obtained from srl cDNA library, from clone srl.pk0162.a9, derived from soybean root library. It has 87% sequence identity to Citrullus lanatus serine O-acetyltransferase. Serine O-acetyltransferase converts serine to O-acetyltserine, that is involved in the formation of cysteine. This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related gen and as markers of traits linked to the gene. This is useful for plant breeding. It is also used to create transgenic plants with altered levels of serine O-acetyltransferase, or found in cell types or
                                                                                     Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                AAG39465 standard; Protein; 312 AA.
                            EP1033405-A2
                                                    Arabidopsis thaliana
                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 48833
                                                                              termination sequence
                                                                                                                                                               18-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    developmental stages in which they are not normally found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 38-39; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid fragment encoding a sulfate assimilation protein in plants, useful as probes to isolate genes encoding homologous proteins from other plant species .
                                                                                                                                                                                                                                                                                                                                                                                                                                            283
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                                                                                                                                                                                                                                                                                                                                  vggkekpskhedvpgesmdhtsfisewsdyii 286
                                                                                                                                                                                                                                                                                                IGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                      deegwvwgqikaearrdaesepalasylystilshsslerslsfhlgnklcsstllstll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 880; DB 21;
Pred. No. 1.9e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                     promoter;
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04-JUN-1999;
07-JUN-1999;
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16-JUN-1999;
17-JUN-1999;
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21-MAY-1999;
24-MAY-1999;
24-MAY-1999;
25-MAY-1999;
                                                       28-JUN-1999;
29-JUN-1999;
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05-MAR-1999;
09-MAR-1999;
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19-MAY-1
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14-JUN-1999;
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06-APR-1999,
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29-MAR-1999;
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99US-0140991.
99US-0141287.
99US-0141842.
99US-0142154.
99US-0142055.
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99US-0139453.
99US-0139492.
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990S-0136782
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990S-0138094
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99US-0131449.
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RESULT 12
AAY93902
ID AAY939
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AC AAY939
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XX
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24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3'.
                 03-OCT-2000
                               AAY93902;
                                               AAY93902 standard; Protein; 312
                                                                                                                                                                                                  108
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                                                                                     NPRKHD-KIPCLIMDQTSYLTEWSDYVI 314
                                                                                                                    tch 51.8%; Score 849.5; DB 21; al Similarity 59.7%; Pred. No. 2.1e-74; 160; Conservative 45; Mismatches 62;
                                                                                                                                                                                                                                                                               99US-0155486.
99US-0156458.
99US-0156458.
99US-0157157.
99US-0157865.
99US-0158232.
99US-0158233.
99US-015929.
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99US-0159330.
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99US-0159637.
99US-0159637.
99US-0159637.
99US-0160761.
99US-0160761.
99US-0160761.
99US-0160763.
                 (first entry)
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99US-0142390.
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99US-014290.
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99US-0144085.
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99US-014433.
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99US-0154703.

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RESULT
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Best Local
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             17-OCT-2000
                                   AAG21076;
                                                   AAG21076 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an isoform of serine acetyltransferase (SAT). The SAT polynucleotide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine serine to 0-acetylserine which is a precursor (by reaction with sulphide) for cysteine, itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with
                                                                                                      285 kptihdeecpgesmdhtsfisewsdyii 312
                                                                                                                           288 NPRKHD-KIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                   165 alalhsrisdvfavdihpaakigkgilldhatgvvvgetavignnvsiihhvtiggtgka
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing production of sulfur-containing compounds, e.g. cysteine methionine, in plants, useful e.g. for improving nutritional value, overexpressing serine acetyltransferase
                                                                                                                                                                                                         168 ALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGVTLGGTGKQ 227
                                                                                                                                                                                                                             Claim 11; Page 51-53; 69pp; French.
                                                                                                                                                                                                                                                   108 SVLEESPEIIESTKODLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-431603/37.
N-PSDB; AAA47174.
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                                                                                                                                                                                                                                                                        45 lwtqikaearrdaeaepalasylystilshsslersisfhlgnklcsstllstllydlf1 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine acetyltransferase; SAT; SAT3'; transgenic plant; cysteine; glutathione; methionine; nutrient value; plant-derived food; glutathione; viral resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2000
                                                                                                                                                                                                                                                                                            48 VWIKMLEEAKSDVKOEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLFELFI 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200036127-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana,
                                                                                                                                                   SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE 287
                                                                                                                                          cgdrhpkigdgcligagatilgnvkigagakvgagsvvlidvpcrgtavgnparlvggke
                                                                                                                                                                                                                                                                                                                             160;
                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                           production of glutathione) to improve resistance to stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lappartient A, Derose R,
                                                                                                                                                                                                                                                                                                                                                                                   312 AA;
          (first entry)
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                                                                                                                                                                                                                                                                                                                               51.8%; Score 849.5; DB 21; Length 312; 59.7%; Pred. No. 2.1e-74;
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                                                    312
                                                    AA.
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or
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19-MAY-1999;
20-MAY-1999;
21-MAY-1999;
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18-JUN-1999;
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07-JUN-1999;
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01-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              termination sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridisation assay; genetic mapping; gene expression control; promoter;
               99US-0139458.
99US-0139459.
99US-0139460.
99US-0139461.
99US-0139462.
99US-0139463.
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99US-0139456.
99US-0139457.
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990S-0138094
990S-0138540
990S-0138847
990S-0139119
990S-0139453
990S-0139453
990S-0139453
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99US-0137528.
99US-0137502.
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99US-0135124.
99US-0135353.
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99US-0132487.
99US-0132863.
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99US-0132048.
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990S-0134219
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99US-0130510.
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99US-0127462
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31-AUG-1999;
01-SEP-1999;
10-SEP-1999;
11-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
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13-OCT-1999;
14-OCT-1999;
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15-OCT-1999;
16-OCT-1999;
17-OCT-1999;
18-OCT-1999;
19-OCT-1999;
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                                                        al similarity
160; Conserv
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990S-0151438.
990S-0151438.
990S-0153070.
990S-0153070.
990S-0153070.
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990S-0169330.
990S-0160761.
990S-0160761.
990S-0160761.
990S-0160815.
990S-0161360.
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59.7%;
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                                    314
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31-JUL-1999;
32-JUL-1999;
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990S-0139817.
990S-0140353.
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990S-0141287.
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                                                                                                                                                                                                                                                                                                                            The present amino acid sequence is the serine O-acetyltransferase, a sulphate assimilation protein from Impatiens balsamia. This is obtained from clone ids.pk030.b6, derived from I balsamia developing seed, O-acetyltransferase. Serine O-acetyltransferase converts serine to O-acetyltransferase. Serine O-acetyltransferase converts serine This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes are markers of traits linked to the gene. This is useful for plant levels of serine O-acetyltransferase, or found in cell types or developmental stages in which they are not normally found.
220 TLGGTGKOSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNP 279
                                              140 wsqnrkplslalqsriadvfsvdihpaarigkgvlldhatgvvigetavignnvsiihhv 199
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                           160 WKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGV 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid fragment encoding a sulfate assimilation protein in plants, useful as probes to isolate genes encoding homologous proteins from other plant species -
                                                                                                                                                       100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Falco SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DUPO ) DU PONT DE NEMOURS & CO E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUL-1999;
                                                                                                      80 tllydlf1gvlssdaslraaavadlraarqrdpactsfshcllnykgflaigagrvahkm 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine O-acetyltransferase; sulphate assimilation; clone ids.pk0030.b6; O-acetylserine; cysteine formation; marker; probe; plant breeding;
                                                                                                                                                                    20 vedaeesgvwsqikaearrdaesepalasylystilshsslaasisfhignkicsstlis 79
                                                                                                                                                                                    42 IEDDDD--VWIKMLEEAKSDVKOEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Impatiens balsamia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Impatiens balsamia serine O-acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY44767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY44767 standard; Protein;
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                   NTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-182432/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ50084
                                                                                                                                                                                                                                                                                                                    294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allen SM,
                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0092833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US15872.
                                                                                                                                                                                                                                                 51.6%; Score 846; DB 21; 57.8%; Pred. No. 4.1e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maxwell CA;
                                                                 51;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                               Length 294;
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                             2; Gaps
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QΥ 밁 Qy

104 ELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQN 163

44 DDDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPSNTLF 103

37 deswywsqikaearrdadaepalasflyatvlshpsldrslafhlanklcsstllstlly 96

Matches 160;

Local

Similarity

50.6%;

Length 303; Indels

4.

Gaps

Conservative

44;

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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
                                                                                                                      The present sequence is the rice serine O-acceyyltransferase, a sulphate assimilation protein. This is obtained from r.c24 cDNA library, clone r1r24.pk0069.all, derived from rice leaf inferced with Magaporthe grisea serine 4360-R-62. It has 728 sequence identily to Citrullus lanatus serine O-acetyltransferase. Serine O-acetyltransferase converts serine to O-acetylserine, that is involved in the formation of cysteine. This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes breeding. It is also used to create transgen. Plants with altered levels of serine O-acetyltransferase, or foun! In cell types or avalance of the plant is developed to create transgen.
                                                                                                               developmental stages in which they are not normally found
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                              Claim 6; Page 35-36; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid fragment encoding \alpha sulfate assimilation protein in plants, useful as probes to isolat. Genes encoding
                                                                                                                                                                                                                                                                                                                                                               homologous proteins from other plant species
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ50085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-182432/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200004167-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant breeding; transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serine O-acetyltransferase; sulphate assimil: ion; O-acetylserine; rice; clone rlr24.pk0069.all; cysteine format on; marker; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rice serine O-acetyltransferase-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY44768 standard; Protein; 303 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 arlvggkdkpnvhadvpgesmdhtsfislwsdfvi 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 ARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 tlggtgkqggdrhpkigdgvligagatilgnvrigegak∴⊣agslvlidvppwttavgnp 259
                                                                                          303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0092833.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US15872.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "Encoded by GCG"
Score 831; DB 2;;
Pred. No. 1.2e-72;
4; Mismatches 63;
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Search completed: August 21, 2001, 12:07:44 Job time: 91 sec